Supplementary Data

Supplementary Tables

Table S1 Shannons Diversity Measures And Comparison To Cow

And Ewe Vaginal Microbiota

Host	Mean	Median	Std. Dev.	Shapiro-	p (Ewes)	p (Cows)
				Wilk (p) ¹	` ` ` ′	,
Ewe	2.87	2.97	1.16	0.130	N/A	0.046*
Cow	3.64	3.93	0.96	0.047†	0.046*	N/A
Human	0.64	0.37	0.59	0.011†	<0.001*	<0.001*
Chimpanzee	2.48	2.51	0.92	0.442	0.312	0.004*
Baboon	2.64	2.82	0.35	0.021†	0.790	0.013*
Howler	2.28	2.58	0.69	0.311	0.176	0.001*
Black Colobus	2.63	2.70	0.58	0.586	0.514	0.016*
Red Colobus	2.45	2.63	1.24	0.098	0.485	0.013*
Mangabey	2.61	2.51	0.53	0.875	0.454	0.013*
Vervet	1.37	1.26	0.56	0.152	<0.001*	<0.001*
Lemur	2.70	2.67	0.22	0.377	0.544	0.011*

^{1.} Data determined to be not normally distributed are indicated with '†'. ² Significant differences between ewe or cow diversity were assessed by two sample t-test for normally distributed data and by Wilcoxin-Mann-Whitney test for data that was not normally distributed. Significance was assessed at p <0.05 and is indicated with a '*'.

Supplementary Figure 1

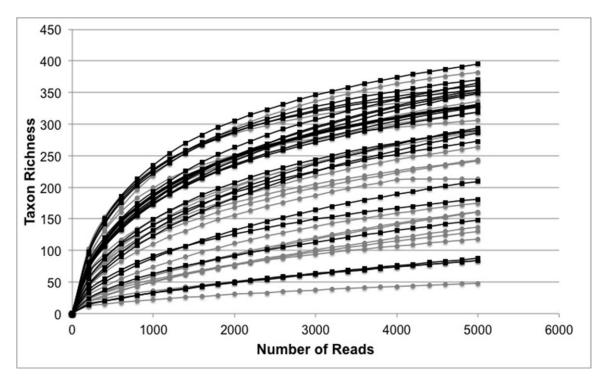


Fig S1. Rarefaction Curve of Detected Taxa in Ewe and Cow Vaginal Tracts Curves from cow vaginal microbiota are shown in black, and ewes in grey.